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SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Levy, Gary
- (ii) TITLE OF INVENTION: Methods of Modulating Immune Coagulation
- (iii) NUMBER OF SEQUENCES: 4
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: BERESKIN & PARR
 - (B) STREET: 40 King Street West
 - (C) CITY: Toronto
 - (D) STATE: Ontario
 - (E) COUNTRY: Canada
 - (F) ZIP: M5H 3Y3
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Gravelle, Micheline
 - (B) REGISTRATION NUMBER: 40,261
 - (C) REFERENCE/DOCKET NUMBER: 9579-006
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (416) 364-7311
 - (B) TELEFAX: (416) 361-1398

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4630 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GATCTAGGGT TGGAAGCCAG GTCTCCTGAG TATGCGAGAA TAAATACAGT CATGGAAGTG	60
TAAAGAGTCT GCCAACATTT TGAGAATGTG AATAGGATTT GGCTAAAATT AAGGGGATAT	120
ACAGAAAAGT CATAGGAAAT CAGGTAAAG ACATAAATAT GAGATAGGCT ACAGAGTGTT	180
TTAAGTAATA CAATAAAACA TTTAGATTTT TGCCCATGTC AGTCATTTTG AAATTATTTT	240
TAAAGCAAAA AAACCCTTTT TAAACAAGAA ATCTTATGAG ATGTCAATAT GCAAAACAAA	300
TTAAAAGGAG GTGGTTTCTC TAACTGAAGC TGTTCTCTT TCCTGCCTTC AGCCTCTGAA	360

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GAGAAAGTTA	GAAAACTATT	ATCATTAAATG	CTACATGTTT	TGAACAAGCT	GATATACCAA	420
GTGGCCCGAGA	GAGCAGGTAG	AAGAACCAGC	GTGGAGACAG	AAAGCAAGAG	GCCCGCCTGC	480
CAGGGCTACC	TGCAGAAAGA	AAGGGCAAAG	ATGCTGTAGG	CAAGAGAAGT	TCAGGACAGA	540
CACTGGCATA	GCTCAAAGAT	TCACATTTGA	GCAGCTGTGG	AAGATGACAG	TACAATTACC	600
AAAATGTCGA	AGGGCAAAGG	AGGCAGCTAC	TGGTTTGTAT	GAAAGACAAT	TATGTCCTTT	660
TAAATGGGTC	TTAGACATTT	AGACATTTAT	ATACACTATG	CTACGGACAA	AGGAATAGAA	720
AGTAGCACTT	TTTTCTCCAC	TAGTTTTCTT	CTCTTTTCA	AGTAGATGAA	GCAAAAGTCA	780
ACTGCAATAG	TCAGAAAGCT	GTACTTTGTT	ACACTTAGAA	ACTTCTAAAA	GTGCTTAAGA	840
TTTCACCTGA	AAGTCCAACA	TGAAGAAAAT	ACAGGCTCCC	CAATGCCCCA	TTCTAAGAAG	900
GAAAAAGGAC	CATTTTCATT	TTAGTAACGT	TTCTGTTCTA	TAGACAGTTT	GGATAACTAG	960
CTCTTACTTT	TTATCTTTAA	AAACTGTTTT	TCCAGTGAAG	TTACGTATAA	TTATTTACTT	1020
CAAGCGTAGT	ATACCAAATT	ACTTTAGAAA	TGCAAGACTT	TTCTTATACT	TCATAAAATA	1080
CATTATGAAA	GTGAATCTTG	TTGGCTGTGT	ACATTTGACT	ATAATAATTT	CAATGCATAT	1140
TATTTCTATT	GAGAGTAAGT	TACAGTTTTT	GGCAAACGTC	GTTTGTATGAG	GGCTATCTCC	1200
TCTTCCTGTG	CGTTTCTAAA	ACTTGTGATG	CAAACGCTCC	CACCCTTTCC	TGGGAACACA	1260
GAAAGCCTGA	CTCAGGCCAT	GGCCGCTATT	AAAGCAGCTC	CAGCCCTGCG	CACTCCCTGC	1320
TGGGGTGAGC	AGCACTGTAA	AGATGAAGCT	GGCTAACTGG	TACTGGCTGA	GCTCAGCTGT	1380
TCTTGCCACT	TACGGTTTTT	TGGTTGTGGC	AAACAATGAA	ACAGAGGAAA	TTAAAGATGA	1440
AAGAGCAAAG	GATGTCTGCC	CAGTGAGACT	AGAAAGCAGA	GGGAAATGCG	AAGAGGCAGG	1500
GGAGTGCCCC	TACCAGGTAA	GCCTGCCCCC	CTTGACTATT	CAGCTCCCGA	AGCAATTCAG	1560
CAGGATCGAG	GAGGTGTTCA	AAGAAGTCCA	AAACCTCAAG	GAAATCGTAA	ATAGTCTAAA	1620
GAAATCTTGC	CAAGACTGCA	AGCTGCAGGC	TGATGACAAC	GGAGACCCAG	GCAGAAACGG	1680
ACTGTTGTTA	CCCAGTACAG	GAGCCCCGGG	AGAGGTTGGT	GATAACAGAG	TTAGAGAATT	1740
AGAGAGTGAG	GTAAACAAGC	TGTCCTCTGA	GCTAAAGAAT	GCCAAAGAGG	AGATCAATGT	1800
ACTTCATGGT	CGCCTGGAGA	AGCTGAATCT	TGTAAATATG	AACAACATAG	AAAATTATGT	1860
TGACAGCAAA	GTGGCAAATC	TAACATTTGT	TGTCAATAGT	TTGGATGGCA	AATGTTCAAA	1920
GTGTCCCAGC	CAAGAACAAA	TACAGTCACG	TCCAGGTATG	TATAATAATG	TTTTCTTATC	1980
ATATGTTTCAT	AAATGTTATA	CAGTCAGAGA	TGTATCTAAA	AGATTAACCT	GAGTCAGTAA	2040
GTTAAATAGA	TGACAGATTA	AGTCTTTTAT	TTATCAAGGT	GCACAGGAAA	AAATAAATAT	2100
CTTCTCAAAT	ATGACCACAT	AAATATGACC	TAATTACAAA	ATCATAGTTA	GTTCTGTATC	2160
CACTGGAAGT	CACTTTCAAT	TTTAAGATCT	TATTTGTTAA	TGCCAGACCT	ACTTGCAAGC	2220
AGAGATTAGA	GGTCCTTTCT	GCTTTATAAC	ATTAGGTTCT	TCTTGTGAGG	CCTTAAGCAT	2280
TTACTAAACA	CCTTCAAGTA	AGTTTAGTAA	AGTTTCATTA	CTGCCATTGA	TTCAATTATC	2340

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AAACTGCTTT	TGTACATATA	AAGAATTCTT	CAGATGCATG	GTTTCTATTA	ACAAGATCCA	2400
ATGCCTTCCT	TTTATTTCCC	CTTCAGTTCA	ACATCTAATA	TATAAAGATT	GCTCTGACTA	2460
CTACGCAATA	GGCAAAAGAA	GCAGTGAGAC	CTACAGAGTT	ACACCTGATC	CCAAAAATAG	2520
TAGCTTTGAA	GTTTACTGTG	ACATGGAGAC	CATGGGGGGA	GGCTGGACAG	TGCTGCAGGC	2580
ACGTCTCGAT	GGGAGCACCA	ACTTCACCAG	AACATGGCAA	GACTACAAAG	CAGGCTTTGG	2640
AAACCTCAGA	AGGGAATTTT	GGCTGGGGAA	CGATAAAATT	CATCTTCTGA	CCAAGAGTAA	2700
GGAAATGATT	CTGAGAATAG	ATCTTGAAGA	CTTTAATGGT	GTGAACTAT	ATGCCTTGTA	2760
TGATCAGTTT	TATGTGGCTA	ATGAGTTTCT	CAAATATCGT	TTACACGTTG	GTAACATATA	2820
TGGCACAGCT	GGAGATGCAT	TACGTTTCAA	CAAACATTAC	AACCACGATC	TGAAGTTTTT	2880
CACCACTCCA	GATAAAGACA	ATGATCGATA	TCCTTCTGGG	AACTGTGGGC	TGTACTACAG	2940
TTCAGGCTGG	TGGTTTGATG	CATGTCTTTC	TGCAAACTTA	AATGGCAAAT	ATTATCACCA	3000
AAAATACAGA	GGTGTCCGTA	ATGGGATTTT	CTGGGGTACC	TGGCCTGGTG	TAAGTGAGGC	3060
ACACCCTGGT	GGCTACAAGT	CCTCCTTCAA	AGAGGCTAAG	ATGATGATCA	GACCCAAGCA	3120
CTTTAAGCCA	TAAATCACTC	TGTTCAATTC	TCCAGGTATT	CGTTATCTAA	TAGGGCAATT	3180
AATTCCTTGT	TTCATATTTT	TCATAGCTAA	AAAATGATGT	CTGACGGCTA	GGTTCTTATG	3240
CTACACAGCA	TTTGAAATAA	AGCTGAAAAA	CAATGCATTT	TAAAGGAGTC	CTTTGTTGTT	3300
ATGCTGTTAT	CCAATGAACA	CTTGCAAGCA	ATTAGCAATA	TTGAGAATTA	TACATTAGAT	3360
TTACAATTCT	TTTAATTTCT	ATTGAAACTT	TTTCTATTGC	TTGTATTACT	TGCTGTATTT	3420
AAAAAATAAT	TGTTGGCTGG	GTGTGGTAGC	TCACGCTGT	AATCCCAGCA	CTTTGGAATG	3480
TCAAGGCAGG	CAGATCACTT	GAGGTCAGGA	GTTTGAGACC	AGCCTGGCCA	AACATGTGAA	3540
ACGCTGTCTC	TATTAAAAAT	ACAAAAATTA	GCCGGGCATG	GTGGTACATG	CCTGTAATCA	3600
ACGCTGTTTA	TTAAAAATAC	AAAAATTAGC	CGGGCATGGT	GGACATGCCT	GTAATCCTAG	3660
TACTTGGGAG	GCTGAGGCAG	GAGAATCGCT	TGAACCTGAG	AGGAAGAGGT	TGCAGTGAGC	3720
CAAGAATGAG	CCACTGCACT	CCAGCATGGG	TGACAGAGAA	AATCTGTCT	CAAACAAAAA	3780
AATAATAAAA	TTTATTCAGT	AGGTGGATT	TACACAAAGT	AATCTGTATT	TGGGCCATGA	3840
TTTAAGCACA	TCTGAAGGTA	TATCACTCTT	TTCAGGCTAT	AATTATTTGG	GTAATCTTCA	3900
TTCTGAGACA	AACTTAATCT	ATATCATTTA	CTTTGCAACA	GAACAACCCT	ACAGCATTTT	3960
GGTTCCAGCA	CTAAGGGAAC	TAATATCTAT	ATAATTAAAC	TTGTTTCAAT	ATCATTCATG	4020
AAATATAAAA	TACTTGTCAT	TTAAACCGTT	TAAAAATGTG	GTAGCATAAT	GTCACCCCAA	4080
AAAGCATTCA	GAAAGCAATG	TAACTGTGAA	GACCAGGGTT	TAAAGGTAAT	TCATTTATAG	4140
TTTATAACTC	CTTAGATGTT	TGATGTTGAA	AACTGCTTTA	ACATGAAAAT	TATCTTCTCT	4200
TGCTCTGTGT	GAACAATAGC	TTTTAATTTA	AGATTGCTCA	CTACTGTACT	AGACTACTGG	4260
TAGGTTTTTT	TGGGGGGGGG	TGGGTAGGGA	TATGTGGGTA	ATGAAGCATT	TACTTACAGG	4320

CTATCATACT CTGAGGCCAA TTTTATCTCC AAAGCAATAA TATCATTAAG TGATTCACTT 4380
 CATAGAAGGC TAAGTTTCTC TAGGACAGAT AGAAAACATG AATTTTGAAA TATATAGAAC 4440
 AGTAGTTAAA ATACTATATA TTTCAACCCT GGCTGGTAGA TTGCTTATTT TACTATCAGA 4500
 AACTAAAAGA TAGATTTTTC CCCAACAGA AGTATCTGTA ATTTTATATA TTCATCAATT 4560
 CTGGAATGCT ATATATAATA TTTAAAAGAC TTTTAAATG TGTTAATTT CATCATCGTA 4620
 AAAAGGGATC 4630

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 439 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Lys Leu Ala Asn Trp Tyr Trp Leu Ser Ser Ala Val Leu Ala Thr
 1 5 10 15
 Tyr Gly Phe Leu Val Val Ala Asn Asn Glu Thr Glu Glu Ile Lys Asp
 20 25 30
 Glu Arg Ala Lys Asp Val Cys Pro Val Arg Leu Glu Ser Arg Gly Lys
 35 40 45
 Cys Glu Glu Ala Gly Glu Cys Pro Tyr Gln Val Ser Leu Pro Pro Leu
 50 55 60
 Thr Ile Gln Leu Pro Lys Gln Phe Ser Arg Ile Glu Glu Val Phe Lys
 65 70 75 80
 Glu Val Gln Asn Leu Lys Glu Ile Val Asn Ser Leu Lys Lys Ser Cys
 85 90 95
 Gln Asp Cys Lys Leu Gln Ala Asp Asp Asn Gly Asp Pro Gly Arg Asn
 100 105 110
 Gly Leu Leu Leu Pro Ser Thr Gly Ala Pro Gly Glu Val Gly Asp Asn
 115 120 125
 Arg Val Arg Glu Leu Glu Ser Glu Val Asn Lys Leu Ser Ser Glu Leu
 130 135 140
 Lys Asn Ala Lys Glu Glu Ile Asn Val Leu His Gly Arg Leu Glu Lys
 145 150 155 160
 Leu Asn Leu Val Asn Met Asn Asn Ile Glu Asn Tyr Val Asp Ser Lys
 165 170 175
 Val Ala Asn Leu Thr Phe Val Val Asn Ser Leu Asp Gly Lys Cys Ser
 180 185 190
 Lys Cys Pro Ser Gln Glu Gln Ile Gln Ser Arg Pro Val Gln His Leu
 195 200 205
 Ile Tyr Lys Asp Cys Ser Asp Tyr Tyr Ala Ile Gly Lys Arg Ser Ser
 210 215 220

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Glu Thr Tyr Arg Val Thr Pro Asp Pro Lys Asn Ser Ser Phe Glu Val
 225 230 235 240
 Tyr Cys Asp Met Glu Thr Met Gly Gly Gly Trp Thr Val Leu Gln Ala
 245 250 255
 Arg Leu Asp Gly Ser Thr Asn Phe Thr Arg Thr Trp Gln Asp Tyr Lys
 260 265 270
 Ala Gly Phe Gly Asn Leu Arg Arg Glu Phe Trp Leu Gly Asn Asp Lys
 275 280 285
 Ile His Leu Leu Thr Lys Ser Lys Glu Met Ile Leu Arg Ile Asp Leu
 290 295 300
 Glu Asp Phe Asn Gly Val Glu Leu Tyr Ala Leu Tyr Asp Gln Phe Tyr
 305 310 315 320
 Val Ala Asn Glu Phe Leu Lys Tyr Arg Leu His Val Gly Asn Tyr Asn
 325 330 335
 Gly Thr Ala Gly Asp Ala Leu Arg Phe Asn Lys His Tyr Asn His Asp
 340 345 350
 Leu Lys Phe Phe Thr Thr Pro Asp Lys Asp Asn Asp Arg Tyr Pro Ser
 355 360 365
 Gly Asn Cys Gly Leu Tyr Tyr Ser Ser Gly Trp Trp Phe Asp Ala Cys
 370 375 380
 Leu Ser Ala Asn Leu Asn Gly Lys Tyr Tyr His Gln Lys Tyr Arg Gly
 385 390 395 400
 Val Arg Asn Gly Ile Phe Trp Gly Thr Trp Pro Gly Val Ser Glu Ala
 405 410 415
 His Pro Gly Gly Tyr Lys Ser Ser Phe Lys Glu Ala Lys Met Met Ile
 420 425 430
 Arg Pro Lys His Phe Lys Pro
 435

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 5403 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CATAAGGCGT GTCTGACAAA TTCTTCATAC ACACATTTCC CCTTGCACA TTCAGTCTGT	60
ATAGGTTATT TCTATAGGAG AAAAAAATA TTCAAATTCC TTGTGCACTG GTAACAGGCA	120
TGAAGGCTCA GCAAAGCCAA TACGTGTTAT GTCCAGTTGG AGACAGTGCC AGGGCCAACA	180
TTCCAGACTT CTCAGATAGA AAGTGC GCCTGCCCTG CTCTGAGAAT TTGAAGAGAG	240
TAGTTCAGTT AGAATTAAGA GGCAGTAGAG AAAAGTCTTG GGAATCTGG TTAGAGATAT	300
AAATATGAGA ACTGGACATG GTGGTACACA CCTGTGATCT CTGTGTTTAG GAGGGAGAGG	360

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CAGAGAGATC AGGAGTTCAA GGCCAGCCTG AGCTACTTGA GACCCAGTCT AAATAAATAA	420
GAGATAGATT ACAGAGTGCC TTTAACTAGT ACAGAGAAAG AATTGGGGT TATCTGTGTC	480
AGTTACGCTG AAATAATTTT TAAGTAATAA AATCCCTTTT AATAAGAAAC CTTATGAGGT	540
CAGTATGCAC AATGAACTTA AGAGAGACCC CCAGCTCCTG AGCTGAGTGA TGGGGAAGGA	600
CAGCCACTGC CTGTGATGTG TGAGTGACGT GCTTCCAAGT GTTTTAACCA CTGACGATTA	660
CATAGCCTGC ACAGTCAGGA GAAAACAGCC GTATTCTCTG CCAGTTCTCT TCCCTTTTAC	720
AAACAGATGA GAGACACACA CAGAGAATCC ATTTAAAGAG CGGACCTTTG TTCTGATTAG	780
GGGCAATTTT AAGTACTTAA GAGTTCACAC AAAGTCTAGC CTTCAAAAAG AAAACAGGTT	840
CCCAAACCTAG GGAGGAAACA GAATCATTTT CATTTTGGTG ACATTTAGTG GGAAGAAGCT	900
CACAGACATT TAGACGTTCC AACTCTTTCC CCACTAGTGG ACCAAGTATA TAATATGGTA	960
TCTTTTGGGC ACTGGTATTA CAACTGTTTT TTAACAAAA GACTTTCCTT GTGCTTTACT	1020
AAAAACCCAG ACGGTGAATC TTGAATACAA TGCGTGCCAC CCACGGCAGG CATTCTATTG	1080
TGCATAGTTT TGA CTGACAG GAGATGACAG CATTGGCTG GCTGCGCTTG CTGAGGACCC	1140
TCTCCTCCTG TGTGGCGTCT GAGACTGTGA TGCAAATGCG CCCGCCCTTT TCTGGGA ACT	1200
CAGAACGCCT GAGTCAGGCG GCGGTGGCTA TTAAAGCGCC TGGTCAGGCT GGGCTGCCGC	1260
ACTGCAAGGA TGAGGCTTCC TGGTTGGTTG TGGCTGAGTT CTGCCGTCTT CGCTGCCTGC	1320
CGAGCGGTGG AGGAGCACAA CCTGACTGAG GGGCTGGAGG ATGCCAGCGC CCAGGCTGCC	1380
TGCCCCGCGA GGCTGGAGGG CAGCGGGAGG TGCGAGGGGA GCCAGTGCCC CTTCCAGCTC	1440
ACCCTGCCCC CGCTGACCAT CCAGCTCCCG CGGCAGCTTG GCAGCATGGA GGAGGTGCTC	1500
AAAGAAGTGC GGACCCTCAA GGAAGCAGTG GACAGTCTGA AGAAATCCTG CCAGGACTGT	1560
AAGTTGCAGG CTGACGACCA TCGAGATCCC GGCGGGAATG GAGGGAATGG AGCAGAGACA	1620
GCCGAGGACA GTAGAGTCCA GGAAGTGGAG AGTCAGGTGA ACAAGCTGTC CTCAGAGCTG	1680
AAGAATGCAA AGGACCAGAT CCAGGGGCTG CAGGGGCGCC TGGAGACGCT CCATCTGGTA	1740
AATATGAA CA ATTGAGAA CTACGTGGAC AACAAAGTGG CAAATCTAAC CGTTGTGGTC	1800
AACAGTTTGG ATGGCAAGTG TTCCAAGTGT CCCAGCCAAG AACACATGCA GTCACAGCCG	1860
GGTAGGTGTA ATGAGGGTCA TACAGTTTGT TCATGAAAGC TGTATAGCCA GATAGTGGCC	1920
ATAAACATTA ACCCGAGGGA GCATAAGTTA GTCAGACTTT CACCTGTTAA GTTATGGCAG	1980
GAGAAACAAG TGTTTTCTCA AATGAGACAA CAGAAATGGT AAATGATCCA CGTACAAAAA	2040
TCCTATTAGT TGTACTCGTT AGAGACCGTC ACTTGCAAGT CTCTAGACCT TCCCTGCTAG	2100
GTCGACCAAC AGACGAGCAG AAACAGATT CCCCCGAAT CTGAACACAT ATTTGAACAC	2160
AGGACAGGTA TGGCAAGGTT CCTGGCTCTG CTTGCTTAGG TCCCTGGGAA TCAGATCTTG	2220
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TCTAGTGAGA ATGGGAGATT TTTATACATG GAAGCATCTC TCCTCTCTCT CTCCTCTCTC	2340

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CTCCCTCCCT	CCCTCTCTCT	CTCTTTGTGT	GCGTGTGTGG	TGGGGATGAG	GACACGTGTA	2460
GAAC TTCGGG	GGTTGAGACT	TAGTGCATAT	GCATCCTCAC	CATTCCAGTT	AGTGAATGTT	2520
AACACTATTT	AAGGTCACAG	ACCTAACAGC	CTTCTGTGTC	CGGATTCCTG	GATTCCCTAGG	2580
ACCTTTGTGG	ATGGGTTGCC	ACACCCTCTG	TGTTTCATCCT	GACTGTGAGG	TCGATGGGAC	2640
ATAGTAGGGA	TAACTTTCAT	TTGGAATCTC	TAGAGATGGT	AGGTCATCAT	GTCATAGAAT	2700
GTTATCACTA	ATGACCAAGA	TAGACACTCA	TGTTTAAGAG	ACATCACAAG	GTGTATATTA	2760
AATATGACAT	GGCATATAAC	TTGTAATGAC	ACAAAAATAT	TCTGTTACCT	ACTTTTCTCC	2820
TAAAAGCTTG	GGACTCTCCA	GAGTTCTAAA	TACATGCAAA	CAGATTATTG	TGTTTTACAG	2880
GAATCTTATA	TTGAACTTTC	TTTACCTGAC	TCAAATTTTA	TTAAAATTAA	CTGGGAACAA	2940
ATAGTTGGTC	TCTAATCTCT	ACAAAAACCA	CCAAATGATT	ACACTGAGCA	TAATTATAAT	3000
CACCTGCTG	CTACGTCTAG	AAACCAAAC	GTGAAATATT	GGCTGACTGT	ATACCTTCCT	3060
AAATAATAAA	TTCAGGATAA	CATTGCCATA	TTATTGGAGA	ACCCCCCT	CCCTTTTAAA	3120
ACTGGAATCA	TTTTATGTCA	ATCTCAGGTG	AAATACGAAT	GGGTTTCAGA	ACAGTGCTGT	3180
GCACTGAAGG	CTGACATTTA	GAACATATAT	AACGATTTCT	GTAAAGTCTG	CTGTAACAAT	3240
TGCTGATTGT	ATCCTAGGAG	ACTTGGACTC	CTCTCAACGT	TAAGGCAGAG	GAATATAATG	3300
GTTATGAGAG	TAAAACTCTC	TGTCAGGTAC	ATCTGGCTTT	CTGTCCCAGC	TCTGTCACTT	3360
AACACTTAGT	TGCGGTGGGA	AAACTCCCTG	ATCTTCCGGG	AGACTAAGTA	ACTGTATAAG	3420
CAAGCTGGCC	GTGATATCCA	CGTCGTAAGG	CTGCTGTGTG	GGTTCAGTGA	AAACTGTTAC	3480
AGTGATTGGC	AGAGTTTCTG	GAGGTCATTG	ACCCTCATTA	AACCTTGCAT	ACACTTATTC	3540
TTACTACTCT	TTGCTGTTAG	TGTTGCCACC	AGGATTGCCA	TTCAAGGCAG	TCCTGTATAC	3600
TTGATAACAC	CAGTTGGTTC	TGAGGCCTTA	GTTAGCATCT	GTTAGCCTGG	TTCAGGAGAG	3660
TGTATCAGAG	CCAGGTTCCCT	CTATCACATA	AACTGTAACG	CAAGTGAATT	GTCCAATTGC	3720
TGTTGAGTCT	GAGAGTCCTT	GAGGTGCATA	GCTTTGACTA	ATAAATCCCC	ATGCTTTTAT	3780
GCTTTTCCTT	CCTCCCTCTT	CCAGTTCAAC	ATCTAATATA	CAAAGATTGT	TCCGACCACT	3840
ACGTGCTAGG	AAGGAGAAGC	AGTGGGGCCT	ACAGAGTTAC	CCCTGATCAC	AGAAACAGCA	3900
GCTTTGAGGT	CTACTGTGAC	ATGGAGACCA	TGGGTGGAGG	CTGGACGGTG	CTGCAGGCTC	3960
GCCTTGATGG	CAGCACCAAC	TTCACCAGAG	AGTGGAAAGA	CTACAAAGCC	GGCTTTGGAA	4020
ACCTTGAACG	AGAATTTTGG	TTGGGCAACG	ATAAAATTCA	TCTTCTGACC	AAGAGTAAGG	4080
AAATGATTTT	GAGAATAGAT	CTTGAAGACT	TTAATGGTCT	CACACTTTAT	GCCTTGATG	4140
ATCAGTTTTA	TGTGGCTAAT	GAATTTCTCA	AATACCGATT	ACACATCGGT	AACTACAATG	4200
GCACGGCAGG	GGATGCCTTG	CGTTTCAGTC	GACACTACAA	CCATGACCTG	AGGTTTTTCA	4260
CAACCCGAGA	CAGAGACAAC	GATCGGTACC	CCTCTGGGAA	CTGTGGGCTC	TATTACAGCT	4320

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CAGGCTGGTG GTTTGATTCA TGTCTCTCTG CCAATTTAAA TGGCAAATAT TACCACCAGA 4380
 AATACAAAGG TGTCCGTAAT GGGATTTTCT GGGGCACCTG GCCTGGTATA AACCAGGCAC 4440
 AGCCAGGTGG CTACAAGTCC TCCTTCAAAC AGGCCAAGAT GATGATTAGG CCCAAGAATT 4500
 TCAAGCCATA AATTGCTAGT GTTCATCTCT CTGGGCACTC ACTATCTAAG AGGACGATGA 4560
 ATTCTTCAG CCCTTTACCA TATGTCTCAG TTTATATTCC TTTCTATGG CTAAACATTT 4620
 CCTTTAAAGC TTTACAGCTT TTAGAATAAA GCTGAAAAGA TCTAAAAGA CTCCTATGTT 4680
 GCTGTTATAT GAGGAATGCT TGAAAGCACT GGAAATATTG ACAATTATAC ATTATAATTG 4740
 CAAAACCTTT CATTTTTATT AGTTGAAAAG TTTCCTAATA TTTTATTAT TTTTATAATA 4800
 AAAACTAAAT TATTCAGCAA GCTAGATTCT ATATACGCAA GTTTTATTTT CACTAGGGCT 4860
 AAATATACAC ATTTGAGAAT ATACCAGTCC TTCCAGGTAC AACTGAAAGC CAAGAACTGT 4920
 AGTATTATCT TTCGTCTAAG AAGAACTTAA AGCATTTTAG TTCTCAAGAA GAAGGGCAGG 4980
 GATGGGATTG GGGGCCAGGG ACAATATGTA TAGCTAAATG TATTCATCTA ATGCAAAATA 5040
 TGGCATTAAT ATACCTAAAA ATGTGGTAGC ATAATATATG TCTCTTCCCT CTCCAATTGA 5100
 AAAATAATGT TACCCTGTAG ACTTTGGTTT AGTGGAATT CACTTACTGT TTATAGCCTG 5160
 TTAGACCGCG ATACAAAAGC TGCTTTATCC TCTCCCTCTG CTCTCTGTGC ACAATGGTTT 5220
 GTGATGTAAG GTGCTAGACT ACTGTAAGGT TTCCTTGGGG AAAGGCATGG TAAGGGAAAA 5280
 CACACTGGTT TATATTTTGA AAGCCAATCC TAATCCCAA GCAATACTGT TGTCGAGGAG 5340
 TCAACGTTCT AGGAAGCTGA CTTTCTAGA ACAAATGTAT TTATTAGGAT GAATTTGGGA 5400
 ATT 5403

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 432 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Arg Leu Pro Gly Trp Leu Trp Leu Ser Ser Ala Val Leu Ala Ala
 1 5 10 15
 Cys Arg Ala Val Glu Glu His Asn Leu Thr Glu Gly Leu Glu Asp Ala
 20 25 30
 Ser Ala Gln Ala Ala Cys Pro Ala Arg Leu Glu Gly Ser Gly Arg Cys
 35 40 45
 Glu Gly Ser Gln Cys Pro Phe Gln Leu Thr Leu Pro Thr Leu Thr Ile
 50 55 60
 Gln Leu Pro Arg Gln Leu Gly Ser Met Glu Glu Val Leu Lys Glu Val
 65 70 75 80

Arg	Thr	Leu	Lys	Glu	Ala	Val	Asp	Ser	Leu	Lys	Lys	Ser	Cys	Gln	Asp
				85					90					95	
Cys	Lys	Leu	Gln	Ala	Asp	Asp	His	Arg	Asp	Pro	Gly	Gly	Asn	Gly	Gly
			100					105					110		
Asn	Gly	Ala	Glu	Thr	Ala	Glu	Asp	Ser	Arg	Val	Gln	Glu	Leu	Glu	Ser
		115					120					125			
Gln	Val	Asn	Lys	Leu	Ser	Ser	Glu	Leu	Lys	Asn	Ala	Lys	Asp	Gln	Ile
	130					135					140				
Gln	Gly	Leu	Gln	Gly	Arg	Leu	Glu	Thr	Leu	His	Leu	Val	Asn	Met	Asp
145					150					155				160	
Asn	Ile	Glu	Asn	Tyr	Val	Asp	Asn	Lys	Val	Ala	Asn	Leu	Thr	Val	Val
				165					170					175	
Val	Asn	Ser	Leu	Asp	Gly	Lys	Cys	Ser	Lys	Cys	Pro	Ser	Gln	Glu	His
			180					185					190		
Met	Gln	Ser	Gln	Pro	Val	Gln	His	Leu	Ile	Tyr	Lys	Asp	Cys	Ser	Asp
		195					200					205			
His	Tyr	Val	Leu	Gly	Arg	Arg	Ser	Ser	Gly	Ala	Tyr	Arg	Val	Thr	Pro
	210					215					220				
Asp	His	Arg	Asn	Ser	Ser	Phe	Glu	Val	Tyr	Cys	Asp	Met	Glu	Thr	Met
225					230					235					240
Gly	Gly	Gly	Trp	Thr	Val	Leu	Gln	Ala	Arg	Leu	Asp	Gly	Ser	Thr	Asn
				245					250					255	
Phe	Thr	Arg	Glu	Trp	Lys	Asp	Tyr	Lys	Ala	Gly	Phe	Gly	Asn	Leu	Glu
			260					265					270		
Arg	Glu	Phe	Trp	Leu	Gly	Asn	Asp	Lys	Ile	His	Leu	Leu	Thr	Lys	Ser
		275					280					285			
Lys	Glu	Met	Ile	Leu	Arg	Ile	Asp	Leu	Glu	Asp	Phe	Asn	Gly	Leu	Thr
	290					295					300				
Leu	Tyr	Ala	Leu	Tyr	Asp	Gln	Phe	Tyr	Val	Ala	Asn	Glu	Phe	Leu	Lys
305					310					315					320
Tyr	Arg	Leu	His	Ile	Gly	Asn	Tyr	Asn	Gly	Thr	Ala	Gly	Asp	Ala	Leu
				325					330					335	
Arg	Phe	Ser	Arg	His	Tyr	Asn	His	Asp	Leu	Arg	Phe	Phe	Thr	Thr	Pro
			340					345					350		
Asp	Arg	Asp	Asn	Asp	Arg	Tyr	Pro	Ser	Gly	Asn	Cys	Gly	Leu	Tyr	Tyr
		355					360					365			
Ser	Ser	Gly	Trp	Trp	Phe	Asp	Ser	Cys	Leu	Ser	Ala	Asn	Leu	Asn	Gly
						375					380				
Lys	Tyr	Tyr	His	Gln	Lys	Tyr	Lys	Gly	Val	Arg	Asn	Gly	Ile	Phe	Trp
385					390					395					400
Gly	Thr	Trp	Pro	Gly	Ile	Asn	Gln	Ala	Gln	Pro	Gly	Gly	Tyr	Lys	Ser
				405					410					415	
Ser	Phe	Lys	Gln	Ala	Lys	Met	Met	Ile	Arg	Pro	Lys	Asn	Phe	Lys	Pro
			420					425					430		